SEQUENCE LISTING

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<120> USE OF LECTIN LIBRARY FOR DISTINGUISHING GLYCOPROTEINS OR CELLS, DIAGNOSING SERUM OR CELLS, OR FRACTIONATING GLYCOPROTEINS OR CELLS

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<141> 2005-08-18

<150> PCT/JP03/10461
<151> 2003-08-19

<150> JP 2002-239979
<151> 2002-08-20

<160> 40

<170> PatentIn Ver. 3.3

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ttc tta act ttc ttc ctt ttg cta ctc aac aac gta aac tca tca gat   96
Phe Leu Thr Phe Phe Leu Leu Leu Leu Asn Asn Val Asn Ser Ser Asp
                  20                  25                  30

gag ctt tct ttt acc atc aac aat ttc atg cca aat caa ggc gat cta   144
Glu Leu Ser Phe Thr Ile Asn Asn Phe Met Pro Asn Gln Gly Asp Leu
             35                  40                  45

ctc ttc caa ggt gta gcc act gtt tca cca aca ggg gta tta caa ctt   192
Leu Phe Gln Gly Val Ala Thr Val Ser Pro Thr Gly Val Leu Gln Leu
         50                  55                  60

acc agc gaa gaa aac ggt caa ccc ctg gag tat tct gtt ggc aga gct   240
Thr Ser Glu Glu Asn Gly Gln Pro Leu Glu Tyr Ser Val Gly Arg Ala
     65                  70                  75
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cta tat act gcc cct gtg cgc att tgg gac agt acc act ggc gcc gta   288
Leu Tyr Thr Ala Pro Val Arg Ile Trp Asp Ser Thr Thr Gly Ala Val
 80                  85                  90                  95

gca agc ttc tcc act tcc ttc acc ttt gtt gtg aaa gca gct agg gga   336
Ala Ser Phe Ser Thr Ser Phe Thr Phe Val Val Lys Ala Ala Arg Gly
                100                 105                 110

gct tct gac ggt tta gcc ttc ttt ctt gca cca cct gat tct cag atc   384
Ala Ser Asp Gly Leu Ala Phe Phe Leu Ala Pro Pro Asp Ser Gln Ile
            115                 120                 125

cct tcg ggc agc gta tcg aaa tac cta gga ctt ttt aac aac tca aat   432
Pro Ser Gly Ser Val Ser Lys Tyr Leu Gly Leu Phe Asn Asn Ser Asn
        130                 135                 140

tcc gat agt tcc aac caa att gtt gct gta gag ttt gac act tac ttc   480
Ser Asp Ser Ser Asn Gln Ile Val Ala Val Glu Phe Asp Thr Tyr Phe
    145                 150                 155

ggc cat agt tat gat ccc tgg gat cca aat tat cga cat atc gga att   528
Gly His Ser Tyr Asp Pro Trp Asp Pro Asn Tyr Arg His Ile Gly Ile
160                 165                 170                 175

gat gtc aac ggt att gag tcg ata aaa act gtg caa tgg gat tgg att   576
Asp Val Asn Gly Ile Glu Ser Ile Lys Thr Val Gln Trp Asp Trp Ile
                180                 185                 190

aac ggc gga gtt gcc ttt gct acc ata acc tat cta gct ccc aac aaa   624
Asn Gly Gly Val Ala Phe Ala Thr Ile Thr Tyr Leu Ala Pro Asn Lys
            195                 200                 205

acg tta ata gca tct cta gtt tac cct tcc aat caa aca agt ttc att   672
Thr Leu Ile Ala Ser Leu Val Tyr Pro Ser Asn Gln Thr Ser Phe Ile
        210                 215                 220

gtc gct gct tct gtt gat ttg aag gga atc ctc cct gag tgg gtt aga   720
Val Ala Ala Ser Val Asp Leu Lys Gly Ile Leu Pro Glu Trp Val Arg
    225                 230                 235

gtt ggt ttc tct gct gcc acg ggt gct cct aaa gca gtt gaa acc cac   768
Val Gly Phe Ser Ala Ala Thr Gly Ala Pro Lys Ala Val Glu Thr His
240                 245                 250                 255

gat gtt cgt tcc tgg tct ttc acg tca act ttg gaa gcc aac agc cct   816
Asp Val Arg Ser Trp Ser Phe Thr Ser Thr Leu Glu Ala Asn Ser Pro
                260                 265                 270

gct gat gtg gat aat aat gtg cat atc gca cgt tac act gca           858
Ala Asp Val Asp Asn Asn Val His Ile Ala Arg Tyr Thr Ala
            275                 280                 285

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aataatggtt atcggcgcag ctatacaaaa at                               950
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             20                  25                  30

Leu Ser Phe Thr Ile Asn Asn Phe Met Pro Asn Gln Gly Asp Leu Leu
         35                  40                  45

Phe Gln Gly Val Ala Thr Val Ser Pro Thr Gly Val Leu Gln Leu Thr
     50                  55                  60

Ser Glu Glu Asn Gly Gln Pro Leu Glu Tyr Ser Val Gly Arg Ala Leu
 65                  70                  75                  80

Tyr Thr Ala Pro Val Arg Ile Trp Asp Ser Thr Thr Gly Ala Val Ala
                 85                  90                  95

Ser Phe Ser Thr Ser Phe Thr Phe Val Val Lys Ala Ala Arg Gly Ala
            100                 105                 110

Ser Asp Gly Leu Ala Phe Phe Leu Ala Pro Pro Asp Ser Gln Ile Pro
        115                 120                 125

Ser Gly Ser Val Ser Lys Tyr Leu Gly Leu Phe Asn Asn Ser Asn Ser
    130                 135                 140

Asp Ser Ser Asn Gln Ile Val Ala Val Glu Phe Asp Thr Tyr Phe Gly
145                 150                 155                 160

His Ser Tyr Asp Pro Trp Asp Pro Asn Tyr Arg His Ile Gly Ile Asp
                165                 170                 175

Val Asn Gly Ile Glu Ser Ile Lys Thr Val Gln Trp Asp Trp Ile Asn
            180                 185                 190

Gly Gly Val Ala Phe Ala Thr Ile Thr Tyr Leu Ala Pro Asn Lys Thr
        195                 200                 205

Leu Ile Ala Ser Leu Val Tyr Pro Ser Asn Gln Thr Ser Phe Ile Val
    210                 215                 220

Ala Ala Ser Val Asp Leu Lys Gly Ile Leu Pro Glu Trp Val Arg Val
225                 230                 235                 240

Gly Phe Ser Ala Ala Thr Gly Ala Pro Lys Ala Val Glu Thr His Asp
                245                 250                 255

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atc 63

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Pro Ser

<210> 35
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